

arranging the comparison results in a square matrix indexed by the plurality of biopolymer materials;

creating a high-dimensional context vector for one of the biopolymer materials based on a row or column of the square matrix; and

creating a comparison matrix based on the context vector to enable visualization of the sequence data of the respective biopolymer material.

15. The method according to claim 14, wherein from each row or column of the square matrix, a respective high-dimensional context vector is created for each of the biopolymer materials based on the comparison results in the row or column.

16. The method according to claim 14, wherein the comparing uses a Basic Local Alignment Search Tool.

17. The method according to claim 14, wherein the comparing provides comparison results based on an expectation of a relation.

19. The method according to claim 14, wherein the biopolymer material is nucleic acid.

20. An apparatus for generating a high-dimensional vector for at least one of a plurality of biopolymer materials represented in a set of sequence data, the apparatus comprising:

at least one memory having program instructions, and
at least one processor configured to execute the program instructions to perform the operations of:

comparing sequence data regarding each biopolymer material to sequence data regarding each other biopolymer material to provide a respective comparison result;

arranging the comparison results in a square matrix indexed by the plurality of biopolymer materials;

creating a high-dimensional context vector for one of the biopolymer materials based on a row or column of the square matrix; and

creating a comparison matrix based on the context vector to enable visualization of the sequence data of the respective biopolymer material.

21. An apparatus for generating a high-dimensional vector for at least one of a plurality of biopolymer materials represented in a set of sequence data, the apparatus comprising:

means for comparing sequence data regarding each biopolymer material to sequence data regarding each other biopolymer material to provide a respective comparison result;

means for arranging the comparison results in a square matrix indexed by the plurality of biopolymer material;

means for creating a high-dimensional context vector for one of the biopolymer materials based on a row or column of the square matrix; and

means for creating a comparison matrix based on the context vector to enable visualization of the sequence data of the respective biopolymer material.

22. A computer-readable medium containing instructions for controlling a computer system to perform a method for generating a high-dimensional vector for at least one of a plurality of biopolymer materials represented in a set of sequence data, the method comprising:

comparing sequence data regarding each biopolymer material to sequence data regarding each other biopolymer material to provide a respective comparison result;

arranging the comparison results in a square matrix indexed by the plurality of biopolymer materials;

creating a high-dimensional context vector for one of the biopolymer materials based on a row or column of the square matrix; and

creating a comparison matrix based on the context vector to enable visualization of the sequence data of the respective biopolymer material.

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and